SEQUENCE LISTING

<110> Quertermous, Thomas
Hogan, Brigid
Snodgrass, Ralph H
Zupancic, Thomas J

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<141> 1999-01-25

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<151> 1996-06-05

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35 40 45

Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
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35 40 45

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35 40 45

Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val Lys
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Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val Ile Pro
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Ser Gln Asp Gly His His Trp Thr Gln Ile Leu Tyr Asn Gly Lys Val
35 40 45

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<212> PRT
<213> Xenopus

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35 40 45

Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val Val Tyr
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Val Thr Trp

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35 40 45

Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro Glu Leu
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Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
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ctcgctcccc tccagctctc gcttcattgt tctccaagtc agaagccccc gcatccgccg    240

cgcagcagcg tgagccgtag tcactgctgg ccgcttcgcc tgcgtgcgcg cacggaaatc    300

ggggagccag gaacccaagg agccgccgtc cgcccgctgt gcctctgcta gaccactcgc    360

agccccagcc tctctcaagc gcacccacct ccgcgcaccc cagctcaggc gaagctggag    420

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agaagcgctg cgggaggaaa gacgtcctct tgatctctga cagggcgggg tttactgctg    540

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cgtccgtgag aagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt       651
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gga ctc agc ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac      699
Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn
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ccg aac ccc tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat      747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp
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gat tcc ttt tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc      795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys
    45                  50                  55

tct agt gtt gtg gag gtt gca tca gat gaa gaa aag cct act tca gca      843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala
60                  65                  70                  75

ggt ccc tgc atc cct aac cca tgc cat aac gga gga acc tgt gag ata      891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile
                80                  85                  90
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agc gaa gcc tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt      939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys
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cct cgg gga ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt      987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys
        110                 115                 120

gaa gct gag cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct     1035
Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala
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aac tac tct tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa     1083
Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln
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tat aaa tgc tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat     1131
Tyr Lys Cys Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn
                160                 165                 170

cag caa atc aca gct tca tct aat cac cga gct ctt ttt gga ctc cag     1179
Gln Gln Ile Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln
            175                 180                 185

aag tgg tat ccc tac tat gct cga ctt aat aag aag ggc ctt ata aat     1227
Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn
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gcc tgg aca gct gct gaa aat gac aga tgg cca tgg att cag ata aat     1275
Ala Trp Thr Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn
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ttg caa aga aaa atg aga gtc act ggt gtt att acc caa gga gca aaa     1323
Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
220                 225                 230                 235

agg att gga agc cca gag tac ata aaa tcc tac aaa att gcc tac agc     1371
Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser
                240                 245                 250

aat gac ggg aag acc tgg gca atg tac aaa gta aaa ggc acc aat gaa     1419
Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
            255                 260                 265

gag atg gtc ttt cgt gga aat gtt gat aac aac aca cca tat gct aat     1467
Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn
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att tgt cga agg cat tgt act tta aga atg gaa ctt ctt ggc tgt gag     1563
Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
300                 305                 310                 315

ctc tca ggc tgt tca gaa cct ttg ggg atg aaa tca ggg cat ata caa     1611
Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
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gac tac cag atc act gcc tcc agc gtc ttc aga aca ctc aac atg gac     1659
Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp
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atg ttt act tgg gaa cca agg aaa gcc agg ctg gac aag caa ggc aaa     1707
Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
        350                 355                 360

gta aat gcc tgg act tcc ggc cat aac gac cag tca caa tgg tta cag     1755
Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
    365                 370                 375

gtt gat ctt ctt gtc cct act aag gtg aca ggc atc att aca caa gga     1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
380                 385                 390                 395

gct aaa gat ttt ggt cac gtg cag ttt gtt ggg tca tac aaa cta gct     1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
                400                 405                 410

tac agc aat gat gga gaa cac tgg atg gtg cac cag gat gaa aaa cag     1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln
            415                 420                 425

agg aaa gac aag gtt ttt caa ggc aat ttt gac aat gac act cac agg     1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
        430                 435                 440

aaa aat gtc atc gac cct ccc atc tat gca cga ttc ata aga atc ctt     1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu
    445                 450                 455

cct tgg tcc tgg tat gga agg atc act ctg cgg tca gag ctg ctg ggc     2043
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Cys Ala Glu Glu Glu
480

tttcctataa gtatctccac gaaatgaact gtgtgaagct gatggaaact gcatttgttt 2158

ttttcaaagt gttcaaatta tggtaggcta ctgactgtct ttttaggagt tctaagcttg 2218

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35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
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Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
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Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
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Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
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Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
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His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

C1

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
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Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
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Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
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Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
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Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
275 280 285

Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
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Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
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Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
325 330 335

Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
340 345 350

Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
355 360 365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
370 375 380

C1

Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
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His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
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Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
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Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
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Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
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Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
        115                 120                 125

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
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Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
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Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
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Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
195 200 205

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
210 215 220

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
225 230 235 240

Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
245 250 255

Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
260 265 270

C1

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
275 280 285

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
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Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
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Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
325 330 335

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
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Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
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370 375 380

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
385 390 395 400

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Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
435 440 445

Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
450 455 460

C1

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
465 470 475 480

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Ser Met Glu

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<210> 18
<211> 4
<212> PRT
<213> Homo sapiens

<400> 18

Arg Cys Phe Tyr
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<210> 19
<211> 318
<212> DNA
<213> mouse

<400> 19
gacagatggc catggattca gataaatttg caaagaaaaa tgagagtcac tggtgttatt 60

acccaaggag caaaaaggat tggaagccca gagtacataa aatcctacaa aattgcctac 120

agcaatgacg ggaagacctg ggcaatgtac aaagtaaaag gcaccaatga agagatggtc 180

tttcgtggaa atgttgataa caacacacca tatgctaatt ctttcacacc cccaatcaaa 240

gctcagtatg taagactcta cccccaaatt tgtcgaaggc attgtacttt aagaatggaa 300

cttcttggct gtgagctc 318

<210> 20
<211> 316
<212> PRT
<213> Homo sapiens

<400> 20

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
1 5 10 15

C1

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
20 25 30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
35 40 45

His Ala Ser Asn Tyr Asp Ser Lys Pro Trp Ile Gln Val Asn Leu Leu
50 55 60

Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg Ala
65 70 75 80

Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu Asp
85 90 95

Gly Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp Lys Glu

100 105 110

Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met Phe Asn
115 120 125

Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser Cys His
130 135 140

Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu His Gly
145 150 155 160

Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp Ser Gln
165 170 175

Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala Phe Gly
180 185 190

Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Leu Ile Asn Ala
195 200 205

C1

Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val Asp Leu
210 215 220

Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asp
225 230 235 240

Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His Ser Asp
245 250 255

Asp Gly Val Gln Trp Thr Val Tyr Glu Glu Gln Gly Ser Ser Lys Val
260 265 270

Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys Asn Ile Phe Glu
275 280 285

Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro Val Ser Trp His
290 295 300

Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
305 310 315

<210> 21
<211> 321
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (225)..(225)
<223> Xaa is Asp

<220>
<221> MISC_FEATURE
<222> (243)..(243)
<223> Xaa is Phe

C1

<220>
<221> MISC_FEATURE
<222> (266)..(266)
<223> Xaa is Tyr

<220>
<221> MISC_FEATURE
<222> (277)..(277)
<223> Xaa is Phe

<400> 21

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
1 5 10 15

Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Leu Trp
20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
35 40 45

Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
50 55 60

Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
65 70 75 80

Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
85 90 95

Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
100 105 110

Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
115 120 125

Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
130 135 140

C1

Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
145 150 155 160

Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
165 170 175

Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
180 185 190

Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
195 200 205

Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
210 215 220

Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
225 230 235 240

Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
245 250 255

Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
260 265 270

Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
275 280 285

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
290 295 300

Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
305 310 315 320

C1 Thr

<210> 22
<211> 25
<212> PRT
<213> Homo sapiens

<400> 22

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile
20 25

<210> 23
<211> 52
<212> PRT

<213> Homo sapiens

<400> 23

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Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1               5                  10                  15

Ala Val Gly Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro
            20                  25                  30

Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr
        35                  40                  45

Ser Ala Gly Pro
    50
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<210> 24
<211> 43
<212> PRT
<213> Homo sapiens

<400> 24

C1

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Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1               5                  10                  15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
            20                  25                  30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
        35                  40
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<210> 25
<211> 35
<212> PRT
<213> Homo sapiens

<400> 25

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Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
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1 5 10 15

Ala Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys
20 25 30

Glu Tyr Lys
35

<210> 26
<211> 40
<212> PRT
<213> Artificial sequence

<220>
<223> consensus EGF-like domain amino acid sequence

<220>
<221> MISC_FEATURE
<222> (2)..(4)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (13)..(25)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (27)..(27)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (31)..(32)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> Xaa is any one of the 20 amino acids

<220>
<221> MISC_FEATURE
<222> (37)..(38)
<223> Xaa is any one of the 20 amino acids

C1

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Xaa is any one of the 20 amino acids

<400> 26

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30

Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

<210> 27

<211> 310
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, g, t, or c

<400> 27
ngtgatattt gtgatcccaa tccatgtgaa aatggaggta tctgtttgcc aggattggct 60

gtaggttcct tttcctgtga gtgtccagat ggcttcacag accccaactg ttctagtgtt 120

gtggaggttg gtccctgcac tcctaatcca tgccataatg gaggaacctg tgaaataagt 180

gaagcatacc gaggggatac attcataggc tatgtttgta aatgtccccg aggatttaat 240

gggattcact gtcagcacaa cataaatgaa tgcgaagttg agccttgcaa aaatggtgga 300

atatgtacag 310

C1

<210> 28
<211> 2308
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (550)..(1212)
<223>

<220>
<221> misc_feature
<222> (1819)..(1821)
<223> n is a, g, t, or c

<400> 28
gaattccggg agggagggta ggggggcggg ccgcgggggc ccaaagccag ctaggctcag 60

tctcacacgc gcgccgccac tgtttgtata tagtgcgctc ctggcctcag gctcgctccc 120

ctccagctct cgcttcattg ttctccaagt cagaagcccc cgcatccgcc gcgcagcagc 180

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gtgagccgta gtcactgctg gccgcttcgc ctgcgtgcgc gcacggaaat cggggagcca    240

ggaacccaag gagccgccgt ccgcccgctg tgcctctgct agaccactcg cagccccagc    300

ctctctcaag cgcacccacc accactcttt tatcgccctt cccaagattt gagaagcgct    360

atcacccttt ctctagggcc accactcttt tatcgccctt cccaagattt gagaagcgct    420

gcgggaggaa agacgtcctc ttgatctctg acagggcggg gtttactgct gtcctgcagg    480

cgcgcctcgc ctactgtgcc ctccgctacg accccggacc agcccaggtc acgtccgtga    540

gaagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt gga ctc agc     591
         Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
         1               5                  10

ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac ccg aac ccc      639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15                  20                  25                  30

tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat gat tcc ttt      687
Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe
                35                  40                  45

tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc tct agt gtt      735
Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val
            50                  55                  60

gtg gag gtt gca tca gat gaa gaa aag cct act tca gca ggt ccc tgc      783
Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys
        65                  70                  75

atc cct aac cca tgc cat aac gga gga acc tgt gag ata agc gaa gcc      831
Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala
    80                  85                  90

tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt cct cgg gga      879
Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly
95                  100                 105                 110

ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt gaa gct gag      927
Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu
                115                 120                 125

cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct aac tac tct      975
Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser
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            130                 135                 140

tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa tat aaa tgc     1023
Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys
        145                 150                 155

tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat cag caa atc     1071
Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile
    160                 165                 170

aca gct tca tct aat cac cga gct ctt ttt gga ctc cag aag tgg tat     1119
Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr
175                 180                 185                 190

ccc tac tat gct aga ctt aat aag aag ggc ctt ata aat gcc tgg aca     1167
Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr
                195                 200                 205

gct gct gaa aat gac aga tgg cca tgg att cag gta aca gtg gga         1212
Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
            210                 215                 220

tgagacaaat ccatttccca aattatcaga atcattatag aagtaggtta gggagaattg   1272

gctgtgattc tttctcatgg ttaaaatgtg atttagttca gaattaacat ggttggaaac   1332

tctaaaaaat gtggaaaaca ggaacattct atgtctgaaa atctgaaaat agcatcaaga   1392

tgaaaacatt ctttagtcat aaatatactc ttttaagtta tagtagagaa aaagatctta   1452

tcatttcata agtggacttt tgggatagca ttggaaatgt aaatgaaata atacctaat    1512

tgaaaaaagt ttattctaaa gtgttaatat ttagcaacag attcagagac aagaaagtaa   1572

caattcaatc tgtgtatttt ttgtgagaaa tagtttccca tgtgcaaata taaagtgcgc   1632

atcatatcat gataatatcc aactgtctgc agaactccct ttcataaatg agagaatttt   1692

aattcatagt gccttatatc ctcatcagcc atctgacttt actacagaag aaaacaatga   1752

aatgatgcat taagtgcttt gctagaagaa acatcatagc aaagctgata gcccacattc   1812

tgtgcannna agcttccaga gcactcgaga aaaagcagaa atgagatgtt ttatgaaaac   1872

cgaaaagata atctgatttc tgtgaaatat acttttgatc atgtggttct ttaagatagt   1932

cactaacaag tcattagtag cagataccaa atgggagaaa atttccagta tactgagggt   1992
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caaggcagtc atgctgaaac tacatgaggt caggaaagtt ttgaaataag gtgattttgg 2052

aaggatacct tcaactggcc tagattttca agaaacagtg taatcaacag ccaaacatga 2112

gaatctagct aacagcattt agaaaaccag aactaagagt gttactgggg aattgcattt 2172

aaatccagta tgagagtttg caaatgccgt attcttctaa ggggtttgtg ccacattttg 2232

ttaccatgga gtcctctgta agaactttat tagataaatc atctttacac tataatttga 2292

ataaaagccg gaattc 2308

<210> 29
<211> 221
<212> PRT
<213> mouse

<220>
<221> misc_feature
<222> (1819)..(1821)
<223> n is a, g, t, or c

<400> 29

C1

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg

85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
115 120 125

Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Val Thr Val Gly
210 215 220

<210> 30
<211> 481
<212> PRT
<213> Homo sapiens

<400> 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu

20 25 30

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
35 40 45

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
50 55 60

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
115 120 125

C1 Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
130 135 140

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
165 170 175

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
195 200 205

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Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
    210                 215                 220

Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
225                 230                 235                 240

Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
                245                 250                 255

Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
            260                 265                 270

Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
        275                 280                 285

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
    290                 295                 300

His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
305                 310                 315                 320

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
                325                 330                 335

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
            340                 345                 350

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
        355                 360                 365

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu
    370                 375                 380

Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe
385                 390                 395                 400
```

C1

Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
405 410 415

Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
420 425 430

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
435 440 445

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
450 455 460

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
465 470 475 480

Glu

<210> 31
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is any one of the 20 amino acids

<400> 31

Xaa Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu
1 5 10 15

Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe
20 25 30

Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Gly Pro Cys Thr Pro

35 40 45

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
50 55 60

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
65 70 75 80

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
85 90 95

Lys Asn Gly Gly Ile Cys Thr
100